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Genome Sequences of Two *Staphylococcus aureus* Ovine Strains That Induce Severe (Strain O11) and Mild (Strain O46) Mastitis[▽]

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***Staphylococcus aureus* is a major etiological agent of mastitis in ruminants. We report here the genome sequences of two ovine strains that were isolated from gangrenous (strain O11) and subclinical (strain O46) ewe mastitis. Both strains belong to the same clonal complex. Despite this close genotypic relationship, the two isolates were shown to reproducibly induce highly divergent types of infections, either severe (O11) or mild (O46) mastitis, in an experimental ewe model.**

Staphylococcus aureus is one of the main pathogens involved in ruminant mastitis. Staphylococcal mastitis severity is highly variable, ranging from subclinical to gangrenous mastitis. Severity partly relies on bacterial factors. *S. aureus* strains isolated from bovine or ovine-caprine hosts differ from human isolates, as revealed previously (3), and genomic data regarding ruminant isolates are still scarce (4, 6). There is thus a need for more genomic data to better understand mastitis and identify bacterial factors involved in the severity of the infection.

We characterized two *S. aureus* ovine strains, which were shown to be clonally related (9) and reproducibly induced severe (strain O11) and mild (strain O46) mastitis in experimental ewe mastitis (8).

We sequenced the two genomes by using an Illumina Genome Analyzer GAII (Fasteris, Geneva, Switzerland).

Base calling was performed with GAPIipeline 1.4.0 software; a total of 27.6 million reads (pass filter) were obtained. After bar code selection, 13.9 and 11.8 million reads of 71 bases in length were obtained for O11 and O46, respectively. Sequence reads were *de novo* assembled with the Edena assembler (5), version 3.0. Assembly resulted in 87 contigs (sum, 2.77 Mbp; N_{50} , 92.2 kbp; maximum, 266 kbp; minimum, 211 bp) and 96 contigs (sum, 2.81 Mbp; N_{50} , 76.5 kbp; maximum, 209 kbp; minimum, 228 bp) for O11 and O46, respectively. (N_{50} is contig size such that 50% of the entire assembly is contained in contigs equal to or larger than this size.) Totals of 2,787 and 2,822 coding sequences were detected for O11 and O46, respectively, by using Glimmer3 (PMID no. 17237039). Sequence comparison and single nucleotide polymorphism

(SNP) calling were performed with MUMmer (7). Over 53% of the genes were assigned to specific subsystem categories by RAST (1). Gene products were submitted to protein location prediction using the software package SurfG+ (2).

The overall O11 and O46 genomes share high similarity to the ED133 genome. The great majority of the genes were common to both strains, except for an additional prophage (containing 42 coding sequences [CDSs]) detected in the O46 genome, which was not found in ED133 either. The putative O46 prophage genes are functionally unknown.

Genome comparison of O11 and O46 showed numerous SNPs (around 1,600 synonymous SNPs and 1,250 nonsynonymous SNPs detected), which were evenly distributed among the contigs and did not correlate with protein location or function. Fifty and 53 truncated genes were found in O11 and O46, respectively. They correspond to point mutations or to insertions and deletions leading to a premature stop codon or causing a frameshift. Among these truncated genes, 37% are involved in cellular machinery, notably in gene regulation (8.7%), iron metabolism (3%), virulence (11%), and proteins of unknown function (36%).

Further analysis of the two genomes is now under way and will be combined to comparative transcriptome and proteome analyses to identify factors that might explain the hypervirulence of O11 in a mastitis context.

Nucleotide sequence accession numbers. The sequences determined in whole-genome shotgun projects have been deposited at DDBJ/EMBL/GenBank under accession no. AEUQ00000000 (O11) and AEUR00000000 (O46). The versions described in this paper are the first versions, AEUQ01000000 and AEUR01000000.

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